

BCS 03-5005\_PCT-SEQUENZPROTOKOLL.ST25  
SEQUENCE LISTING

&lt;110&gt; Bayer CropScience GmbH

&lt;120&gt; Plants with increased activity of a Class 3 branching enzyme

&lt;130&gt; BCS 03-5005-PCT

&lt;150&gt; EP 03090324.9

&lt;151&gt; 2003-09-30

&lt;160&gt; 6

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 1004

&lt;212&gt; DNA

&lt;213&gt; Solanum tuberosum

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## BCS 03-5005\_PCT-SEQUENZPROTOKOLL.ST25

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Ser	Ile	Arg	Ile	Ser	Ser	Pro	Leu	Ser	Asp	Ser	Arg	Leu	Ser	Phe	Leu		
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Pro	Pro	Gln	Arg	Arg	Lys	Gln	Arg	Pro	Glu	Lys	Tyr	Lys	Gln	Ser	Glu		
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gaa	gag	aaa	gga	atc	gat	cct	gtt	gga	ttt	ctc	agc	aaa	tac	ggc	att	356	
Glu	Glu	Lys	Gly	Ile	Asp	Pro	Val	Gly	Phe	Leu	Ser	Lys	Tyr	Gly	Ile		
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## BCS 03-5005\_PCT-SEQUENZPROTOKOLL.ST25

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Thr His Lys Ala Phe Ala Gln Phe Leu Arg Glu Arg Tyr Lys Ser Leu	
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Lys Asp Leu Lys Asp Glu Ile Leu Thr Arg His Phe Ser Leu Lys Glu	
105 110 115	
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Met Ser Thr Gly Tyr Glu Leu Met Gly Met His Arg Asn Ile Gln His	
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Tyr Asn Tyr Ala Glu Asp Tyr Asp Lys Gly Asp Thr Gly Ile Thr Val	
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Glu Met Phe Gly Pro Asn Gly Pro Gln Thr Glu Glu Glu Leu Glu Ala	
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## BCS 03-5005\_PCT-SEQUENZPROTOKOLL.ST25

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gtg Val 615	gat Asp	gca Ala	act Thr	ctg Leu	tat Tyr 620	cct Pro	gga Gly	ctc Leu	tgc Cys	gat Asp 625	cca Pro	aca Thr	tct Ser	caa Gln	ggt Gly 630	1988

## BCS 03-5005\_PCT-SEQUENZPROTOKOLL.ST25

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gag tca tta ctt aga ggc tgc tcg tta cac aag atg atc aga tta att Glu Ser Leu Leu Arg Gly Cys Ser Leu His Lys Met Ile Arg Leu Ile 715 720 725	2276
aca tct aca att ggt ggt cat gca tac ctc aac ttc atg ggc aat gaa Thr Ser Thr Ile Gly Gly His Ala Tyr Leu Asn Phe Met Gly Asn Glu 730 735 740	2324
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cca agt aga agt gct cag gtc tac aag ttg acc cga att cta aga gca Pro Ser Arg Ser Ala Gln Val Tyr Lys Leu Thr Arg Ile Leu Arg Ala 890 895 900	2804

## BCS 03-5005\_PCT-SEQUENZPROTOKOLL.ST25

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&lt;211&gt; 902

&lt;212&gt; PRT

&lt;213&gt; solanum tuberosum

&lt;400&gt; 4

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Leu Lys Phe Val Arg Ser Arg Arg Ala Arg Val Ser Arg Cys Arg Cys  
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Ser Ala Thr Glu Gln Pro Pro Pro Gln Arg Arg Lys Gln Arg Pro Glu  
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Lys Tyr Lys Gln Ser Glu Glu Glu Lys Gly Ile Asp Pro Val Gly Phe  
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Leu Ser Lys Tyr Gly Ile Thr His Lys Ala Phe Ala Gln Phe Leu Arg  
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Glu Arg Tyr Lys Ser Leu Lys Asp Leu Lys Asp Glu Ile Leu Thr Arg  
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His Phe Ser Leu Lys Glu Met Ser Thr Gly Tyr Glu Leu Met Gly Met  
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His Arg Asn Ile Gln His Arg Val Asp Phe Leu Glu Trp Ala Pro Gly  
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Ala Arg Tyr Cys Ala Leu Ile Gly Asp Phe Asn Gly Trp Ser Thr Thr  
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BCS 03-5005\_PCT-SEQUENZPROTOKOLL.ST25

Gly Asn Cys Ala Arg Glu Gly His Phe Gly His Asp Asp Tyr Gly Tyr  
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Trp Phe Ile Ile Leu Glu Asp Lys Leu Arg Glu Gly Glu Glu Pro Asp  
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Lys Leu Tyr Phe Gln Gln Tyr Asn Tyr Ala Glu Asp Tyr Asp Lys Gly  
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Asp Thr Gly Ile Thr Val Glu Glu Ile Phe Lys Lys Ala Asn Asp Glu  
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Trp Lys Glu Gln Gln Lys Lys Asp Pro Ala Ser Asn Leu Pro Ser Tyr  
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Tyr Trp Leu Glu Thr Lys Lys Gly Arg Lys Gly Trp Leu Gln Lys Tyr  
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Met Pro Ala Leu Pro His Gly Ser Lys His Arg Val Tyr Phe Asn Thr  
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Pro Asn Gly Pro Leu Glu Arg Val Pro Ala Trp Ala Asn Phe Val Ile  
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Pro Asp Ala Asp Gly Met Ala Leu Ala Val His Trp Glu Pro Pro Pro  
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Leu Arg Ile Tyr Glu Cys His Val Gly Ile Ser Gly Gln Glu Pro Lys  
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Val Ser Ser Phe Asn Asp Phe Ile Ser Lys Val Leu Pro His Val Lys  
420 425 430



## BCS 03-5005\_PCT-SEQUENZPROTOKOLL.ST25

Glu Ala Gly Tyr Asn Ala Thr Gln Ile Ile Gly Val Val Glu His Lys  
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Asp Tyr Phe Thr Val Gly Tyr Arg Val Thr Asn Phe Tyr Ala Val Ser  
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Ser Arg Tyr Gly Thr Pro Asp Asp Phe Lys Arg Leu Val Asp Glu Ala  
 465 470 475 480

His Gly Leu Gly Leu Leu Val Phe Leu Glu Ile Val His Ser Tyr Ala  
 485 490 495

Ala Ala Asp Glu Met Val Gly Leu Ser Leu Phe Asp Gly Ala Asn Asp  
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Cys Tyr Phe His Thr Gly Lys Arg Gly His His Lys Phe Trp Gly Thr  
 515 520 525

Arg Met Phe Lys Tyr Gly Asp Pro Asp Val Leu His Phe Leu Leu Ser  
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Asn Leu Asn Trp Trp Val Glu Glu Tyr His Val Asp Gly Phe His Phe  
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His Ser Leu Ser Ser Met Leu Tyr Thr His Asn Gly Phe Ala Ser Phe  
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Thr Gly Asp Met Asp Glu Tyr Cys Asn Gln Tyr Val Asp Lys Glu Ala  
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Leu Leu Tyr Leu Ile Leu Ala Asn Glu Val Leu His Ala Leu His Pro  
 595 600 605

Asn Val Ile Thr Ile Ala Val Asp Ala Thr Leu Tyr Pro Gly Leu Cys  
 610 615 620

Asp Pro Thr Ser Gln Gly Gly Leu Gly Phe Asp Tyr Phe Ala Asn Leu  
 625 630 635 640

Ser Ala Ser Glu Met Trp Leu Ala Leu Leu Glu Asn Thr Pro Asp His  
 645 650 655

Glu Trp Cys Met Ser Lys Ile Val Ser Thr Leu Val Gly Asp Arg Gln  
 660 665 670

Asn Thr Asp Lys Met Leu Leu Tyr Ala Glu Asn His Asn Gln Ser Ile  
 675 680 685

Ser Gly Gly Arg Ser Phe Ala Glu Ile Leu Ile Gly Asn Ser Leu Gly  
 690 695 700

## BCS 03-5005\_PCT-SEQUENZENPROTOKOLL.ST25

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Lys Met Ile Arg Leu Ile Thr Ser Thr Ile Gly Gly His Ala Tyr Leu  
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Asn Phe Met Gly Asn Glu Phe Gly His Pro Lys Arg Val Glu Phe Pro  
 740 745 750

Met Ser Ser Asn Asn Phe Ser Phe Ser Leu Ala Asn Arg Arg Trp Asp  
 755 760 765

Leu Leu Glu Asp Val Val His Tyr Gln Leu Phe Ser Phe Asp Lys Asp  
 770 775 780

Met Met Asp Leu Asp Lys Asn Gly Arg Ile Leu Ser Arg Gly Leu Ala  
 785 790 795 800

Asn Ile His His Val Asn Asp Thr Thr Met Val Ile Ser Tyr Leu Arg  
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Gly Pro Asn Leu Phe Val Phe Asn Phe His Pro Val Asn Ser Tyr Glu  
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Asn Thr Asp Glu Asn Lys Tyr Gly Gly Arg Gly Leu Leu Gly His Asp  
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Gln Asn Thr Gln Arg Thr Ile Ser Arg Arg Ala Asp Gly Met Arg Phe  
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Met	Leu	Ser	Leu	Ser	Asp	Ser	Ile	Arg	Ile	Ser	Ser	Pro	Leu	Ser		
1				5					10					15		
gat	tct	cgt	ctt	agt	ttt	cta	tct	caa	acc	gga	agc	aga	acc	agt	cgc	97
Asp	Ser	Arg	Leu	Ser	Phe	Leu	Ser	Gln	Thr	Gly	Ser	Arg	Thr	Ser	Arg	
			20					25						30		
cag	ctt	aaa	ttt	gtt	cgc	agc	cgc	cgg	gct	cga	gtt	tcg	agg	tgt	aga	145
Gln	Leu	Lys	Phe	Val	Arg	Ser	Arg	Arg	Ala	Arg	Val	Ser	Arg	Cys	Arg	
			35					40					45			
tgc	tca	gca	acg	gag	caa	ccg	cca	ccg	caa	cga	cgg	aag	caa	cga	ccg	193
Cys	Ser	Ala	Thr	Glu	Gln	Pro	Pro	Pro	Gln	Arg	Arg	Lys	Gln	Arg	Pro	
		50				55						60				
gag	aag	tac	aaa	cag	tcg	gag	gaa	ggg	aaa	gga	atc	gat	cct	gtt	gga	241
Glu	Lys	Tyr	Lys	Gln	Ser	Glu	Glu	Gly	Lys	Gly	Ile	Asp	Pro	Val	Gly	
	65				70						75					
ttt	ctc	agc	aaa	tac	ggc	att	act	cat	aaa	gcg	ttt	gct	caa	ttt	ctt	289
Phe	Leu	Ser	Lys	Tyr	Gly	Ile	Thr	His	Lys	Ala	Phe	Ala	Gln	Phe	Leu	
	80				85					90					95	
cgt	gaa	aga	tat	aaa	tca	ttg	aag	gac	ttg	aag	gat	gaa	ata	ttg	act	337
Arg	Glu	Arg	Tyr	Lys	Ser	Leu	Lys	Asp	Leu	Lys	Asp	Glu	Ile	Leu	Thr	
				100					105					110		
cgt	cat	ttc	agt	ctc	aag	gag	atg	tct	act	ggg	tat	gaa	tta	atg	ggt	385
Arg	His	Phe	Ser	Leu	Lys	Glu	Met	Ser	Thr	Gly	Tyr	Glu	Leu	Met	Gly	
			115					120					125			
atg	cat	cgc	aac	ata	caa	cat	cga	gtg	gat	ttc	ttg	gaa	tggt	gct	cca	433
Met	His	Arg	Asn	Ile	Gln	His	Arg	Val	Asp	Phe	Leu	Glu	Trp	Ala	Pro	
		130					135					140				
ggt	gct	cgc	tac	tgt	gct	ctg	att	ggt	gac	ttc	aat	ggg	tggt	tca	aca	481
Gly	Ala	Arg	Tyr	Cys	Ala	Leu	Ile	Gly	Asp	Phe	Asn	Gly	Trp	Ser	Thr	
	145					150					155					
act	ggt	aac	tgt	gcc	aga	gag	ggt	cat	ttt	ggt	cat	gac	gat	tat	ggg	529
Thr	Gly	Asn	Cys	Ala	Arg	Glu	Gly	His	Phe	Gly	His	Asp	Asp	Tyr	Gly	
	160			165						170					175	
tat	tggt	ttt	att	att	ctt	gaa	gat	aaa	tta	cgt	gaa	gga	gaa	gaa	cct	577
Tyr	Trp	Phe	Ile	Ile	Leu	Glu	Asp	Lys	Leu	Arg	Glu	Gly	Glu	Glu	Pro	
				180					185					190		
gat	aaa	ttg	tat	ttt	caa	cag	tac	aat	tat	gcg	gag	gac	tat	ggt	aaa	625
Asp	Lys	Leu	Tyr	Phe	Gln	Gln	Tyr	Asn	Tyr	Ala	Glu	Asp	Tyr	Gly	Lys	
			195					200					205			
ggt	gac	acg	ggt	att	acc	gtc	gag	gaa	atc	ttt	aaa	aaa	gca	aat	gat	673
Gly	Asp	Thr	Gly	Ile	Thr	Val	Glu	Glu	Ile	Phe	Lys	Lys	Ala	Asn	Asp	
		210					215					220				
gag	tat	tggt	gaa	cct	gga	gaa	gat	cgc	ttc	att	aaa	tca	cgt	tat	gag	721
Glu	Tyr	Trp	Glu	Pro	Gly	Glu	Asp	Arg	Phe	Ile	Lys	Ser	Arg	Tyr	Glu	
	225					230					235					
gtg	gca	gca	aag	tta	tat	gag	gaa	atg	ttc	gga	cca	aat	gga	cct	caa	769
Val	Ala	Ala	Lys	Leu	Tyr	Glu	Glu	Met	Phe	Gly	Pro	Asn	Gly	Pro	Gln	
					245					250					255	

## BCS 03-5005\_PCT-SEQUENZPROTOKOLL.ST25

aca gaa gag gaa cta gaa gca atg cct gat gca gct aca cga tac aaa Thr Glu Glu Glu Leu Glu Ala Met Pro Asp Ala Ala Thr Arg Tyr Lys 260 265 270	817
act tgg aaa gag caa caa aaa gag gat ccg gca agc aat ttg cca tcg Thr Trp Lys Glu Gln Gln Lys Glu Asp Pro Ala Ser Asn Leu Pro Ser 275 280 285	865
tat gat gtg gta gat agt gga aaa gaa tat gat att tac aat att ata Tyr Asp Val Val Asp Ser Gly Lys Glu Tyr Asp Ile Tyr Asn Ile Ile 290 295 300	913
ggt gat cct gaa tcg ttt aag aaa ttt cgt atg aaa cag cct cct att Gly Asp Pro Glu Ser Phe Lys Lys Phe Arg Met Lys Gln Pro Pro Ile 305 310 315	961
gct tac tgg tta gaa act aaa aag gga agg aaa ggc tgg tta cag aaa Ala Tyr Trp Leu Glu Thr Lys Lys Gly Arg Lys Gly Trp Leu Gln Lys 320 325 330 335	1009
tat atg cct gct tta cct cat gga agc aaa tac agg gtg tat ttt aac Tyr Met Pro Ala Leu Pro His Gly Ser Lys Tyr Arg Val Tyr Phe Asn 340 345 350	1057
aca cca aat ggg cct ctt gaa cga gtt cct gcg tgg gcc aat ttt gtc Thr Pro Asn Gly Pro Leu Glu Arg Val Pro Ala Trp Ala Asn Phe Val 355 360 365	1105
att cca gat gca ggc ggg atg gca tta gca gtc cat tgg gaa cca cct Ile Pro Asp Ala Gly Gly Met Ala Leu Ala Val His Trp Glu Pro Pro 370 375 380	1153
cct gaa tat gct tat aaa tgg aaa cac aag cta cca gtc aag cct aag Pro Glu Tyr Ala Tyr Lys Trp Lys His Lys Leu Pro Val Lys Pro Lys 385 390 395	1201
tcc ttg cgc ata tat gaa tgt cat gtt ggc atc tct ggc cag gaa cca Ser Leu Arg Ile Tyr Glu Cys His Val Gly Ile Ser Gly Gln Glu Pro 400 405 410 415	1249
aaa gtt tca tct ttc aat gat ttt att agc aag gtc ctt ccg cat gta Lys Val Ser Ser Phe Asn Asp Phe Ile Ser Lys Val Leu Pro His Val 420 425 430	1297
aaa gaa gct gga tac aat gca ata caa att att gga gtt gtt gag cac Lys Glu Ala Gly Tyr Asn Ala Ile Gln Ile Ile Gly Val Val Glu His 435 440 445	1345
aag gat tat ttc act gtt gga tat aga gtg acc aat ttt tat gct gtt Lys Asp Tyr Phe Thr Val Gly Tyr Arg Val Thr Asn Phe Tyr Ala Val 450 455 460	1393
agt agc cgt tat ggc aca ccg gat gac ttc aag cgc ttg gtt gat gaa Ser Ser Arg Tyr Gly Thr Pro Asp Asp Phe Lys Arg Leu Val Asp Glu 465 470 475	1441
gca cat ggg ctt gga ctg ctt gtc ttt ttg gag att gtg cac tct tat Ala His Gly Leu Gly Leu Leu Val Phe Leu Glu Ile Val His Ser Tyr 480 485 490 495	1489
gca gca gca gat gaa atg gtt ggg tta tct ctt ttt gat gga gca aat Ala Ala Ala Asp Glu Met Val Gly Leu Ser Leu Phe Asp Gly Ala Asn 500 505 510	1537
gat tgc tat ttc cac act ggt aaa cgt gga cac cac aaa ttc tgg ggc Asp Cys Tyr Phe His Thr Gly Lys Arg Gly His His Lys Phe Trp Gly 515 520 525	1585

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aca	cgg	atg	ttc	aaa	tat	gga	gat	ctt	gat	gtt	ctg	cac	ttt	ctt	ctt	1633
Thr	Arg	Met	Phe	Lys	Tyr	Gly	Asp	Leu	Asp	Val	Leu	His	Phe	Leu	Leu	
		530					535					540				
tca	aat	ctg	aac	tgg	tgg	gtg	gag	gag	tat	cat	gtc	gat	ggc	ttc	cat	1681
Ser	Asn	Leu	Asn	Trp	Trp	Val	Glu	Glu	Tyr	His	Val	Asp	Gly	Phe	His	
		545				550					555					
ttt	cat	tcg	ctc	tcg	tcc	atg	ttg	tat	acg	cat	aat	gga	ttt	gct	tca	1729
Phe	His	Ser	Leu	Ser	Ser	Met	Leu	Tyr	Thr	His	Asn	Gly	Phe	Ala	Ser	
		560				565				570					575	
ttt	act	ggt	gac	atg	gat	gaa	tac	tgt	aac	caa	tat	gtt	gac	aag	gag	1777
Phe	Thr	Gly	Asp	Met	Asp	Glu	Tyr	Cys	Asn	Gln	Tyr	Val	Asp	Lys	Glu	
				580					585					590		
gcc	tta	ttg	tac	ctc	ata	tta	gca	aat	gaa	gta	tta	cat	gct	ctt	cat	1825
Ala	Leu	Leu	Tyr	Leu	Ile	Leu	Ala	Asn	Glu	Val	Leu	His	Ala	Leu	His	
			595					600					605			
cct	aat	gtg	atc	acg	att	gct	gag	gat	gca	act	ctg	tat	cct	gga	ctc	1873
Pro	Asn	Val	Ile	Thr	Ile	Ala	Glu	Asp	Ala	Thr	Leu	Tyr	Pro	Gly	Leu	
		610					615					620				
tgc	gat	cca	aca	tct	caa	ggt	gga	ctg	ggc	ttt	gat	tat	ttt	gcc	aat	1921
Cys	Asp	Pro	Thr	Ser	Gln	Gly	Gly	Leu	Gly	Phe	Asp	Tyr	Phe	Ala	Asn	
		625				630					635					
ctt	tct	gcc	tca	gag	atg	tgg	ctt	gca	tta	ctt	gaa	aat	act	cct	gat	1969
Leu	Ser	Ala	Ser	Glu	Met	Trp	Leu	Ala	Leu	Leu	Glu	Asn	Thr	Pro	Asp	
		640				645				650					655	
cat	gaa	tgg	tgc	atg	agt	aag	att	gtt	agc	aca	tta	gtg	ggc	gat	aga	2017
His	Glu	Trp	Cys	Met	Ser	Lys	Ile	Val	Ser	Thr	Leu	Val	Gly	Asp	Arg	
				660					665					670		
caa	aat	act	gat	aaa	atg	ctt	ttg	tat	gca	gaa	aat	cac	aac	cag	tcc	2065
Gln	Asn	Thr	Asp	Lys	Met	Leu	Leu	Tyr	Ala	Glu	Asn	His	Asn	Gln	Ser	
			675					680					685			
att	tct	gga	ggt	cgt	tcc	ttc	gca	gaa	ata	ctg	att	ggt	aac	tcc	ttg	2113
Ile	Ser	Gly	Gly	Arg	Ser	Phe	Ala	Glu	Ile	Leu	Ile	Gly	Asn	Ser	Leu	
		690					695					700				
ggg	aaa	tcc	tcc	ata	tca	caa	gag	tca	tta	ctt	aga	ggc	tgc	tcg	tta	2161
Gly	Lys	Ser	Ser	Ile	Ser	Gln	Glu	Ser	Leu	Leu	Arg	Gly	Cys	Ser	Leu	
		705				710					715					
cac	aag	atg	atc	aga	tta	att	aca	tct	aca	att	ggt	ggt	cat	gca	tac	2209
His	Lys	Met	Ile	Arg	Leu	Ile	Thr	Ser	Thr	Ile	Gly	Gly	His	Ala	Tyr	
		720			725					730					735	
ctc	aac	ttc	atg	ggc	aat	gaa	ttt	ggt	cac	cca	aag	aga	gta	gag	ttt	2257
Leu	Asn	Phe	Met	Gly	Asn	Glu	Phe	Gly	His	Pro	Lys	Arg	Val	Glu	Phe	
				740					745					750		
cca	atg	tca	agc	aac	aat	ttc	tcc	ttt	tca	ctg	gct	aac	cgt	cgc	tgg	2305
Pro	Met	Ser	Ser	Asn	Asn	Phe	Ser	Phe	Ser	Leu	Ala	Asn	Arg	Arg	Trp	
			755					760					765			
gat	cta	ttg	gaa	gat	gtt	gta	cat	tat	caa	ttg	ttc	tca	ttt	gat	aag	2353
Asp	Leu	Leu	Glu	Asp	Val	Val	His	Tyr	Gln	Leu	Phe	Ser	Phe	Asp	Lys	
		770					775					780				
ggt	atg	atg	gac	ttg	gat	aaa	aat	ggg	aga	att	ttg	tcc	aga	ggt	ctt	2401
Gly	Met	Met	Asp	Leu	Asp	Lys	Asn	Gly	Arg	Ile	Leu	Ser	Arg	Gly	Leu	
		785				790					795					

## BCS 03-5005\_PCT-SEQUENZPROTOKOLL.ST25

gcc aac att cac cat gtc aat gat act acc atg gtg att tct tac ttg 2449  
 Ala Asn Ile His His Val Asn Asp Thr Thr Met Val Ile Ser Tyr Leu  
 800 805 810 815  
 aga ggt ccc aat ctc ttt gtg ttc aac ttt cat cct gtc aat tca tat 2497  
 Arg Gly Pro Asn Leu Phe Val Phe Asn Phe His Pro Val Asn Ser Tyr  
 820 825 830  
 gaa aga tac att ata ggt gtg gaa gaa gct gga gag tat caa gtc aca 2545  
 Glu Arg Tyr Ile Ile Gly Val Glu Glu Ala Gly Glu Tyr Gln Val Thr  
 835 840 845  
 tta aat aca gat gaa aac aag tat ggt ggt aga gga cta ctt ggc cat 2593  
 Leu Asn Thr Asp Glu Asn Lys Tyr Gly Gly Arg Gly Leu Leu Gly His  
 850 855 860  
 gat cag aat att caa aga acc att agt aga aga gct gat gga atg aga 2641  
 Asp Gln Asn Ile Gln Arg Thr Ile Ser Arg Arg Ala Asp Gly Met Arg  
 865 870 875  
 ttt tgc ttg gaa gtg cct ctg cca agt aga agt gct cag gtc tac aag 2689  
 Phe Cys Leu Glu Val Pro Leu Pro Ser Arg Ser Ala Gln Val Tyr Lys  
 880 885 890 895  
 ttg acc cga att cta aga gca tgatcactct agtaatcaaa gtgcctcata 2740  
 Leu Thr Arg Ile Leu Arg Ala  
 900  
 tgatgacaca aaaggaaagg ttctacattg cccttacact gatcaatatt gacacctttc 2800  
 cgagggtgagt ttctgtgatt cttgagcaga ctgttggtgta gtcaattatc atgaactttt 2860  
 gccttcagca tccggatagt cgcttctcct gtgcaatgag ggcatggacg aatttttttt 2920  
 tggcttgta tgggggtcat aagcatccgc cagattaaga ttccacaggc ctcgagtaaa 2980  
 accatcactt actttaagga tacacaaaca caccaacggg gtgcaggctc tgataccttc 3040  
 taaagtg 3047

&lt;210&gt; 6

&lt;211&gt; 902

&lt;212&gt; PRT

&lt;213&gt; solanum tuberosum

&lt;400&gt; 6

Met Leu Ser Leu Ser Asp Ser Ile Arg Ile Ser Ser Pro Leu Ser Asp  
 1 5 10 15

Ser Arg Leu Ser Phe Leu Ser Gln Thr Gly Ser Arg Thr Ser Arg Gln  
 20 25 30

Leu Lys Phe Val Arg Ser Arg Arg Ala Arg Val Ser Arg Cys Arg Cys  
 35 40 45

Ser Ala Thr Glu Gln Pro Pro Pro Gln Arg Arg Lys Gln Arg Pro Glu  
 50 55 60

## BCS 03-5005\_PCT-SEQUENZPROTOKOLL.ST25

Lys Tyr Lys Gln Ser Glu Glu Gly Lys Gly Ile Asp Pro Val Gly Phe  
65 70 75 80

Leu Ser Lys Tyr Gly Ile Thr His Lys Ala Phe Ala Gln Phe Leu Arg  
85 90 95

Glu Arg Tyr Lys Ser Leu Lys Asp Leu Lys Asp Glu Ile Leu Thr Arg  
100 105 110

His Phe Ser Leu Lys Glu Met Ser Thr Gly Tyr Glu Leu Met Gly Met  
115 120 125

His Arg Asn Ile Gln His Arg Val Asp Phe Leu Glu Trp Ala Pro Gly  
130 135 140

Ala Arg Tyr Cys Ala Leu Ile Gly Asp Phe Asn Gly Trp Ser Thr Thr  
145 150 155 160

Gly Asn Cys Ala Arg Glu Gly His Phe Gly His Asp Asp Tyr Gly Tyr  
165 170 175

Trp Phe Ile Ile Leu Glu Asp Lys Leu Arg Glu Gly Glu Glu Pro Asp  
180 185 190

Lys Leu Tyr Phe Gln Gln Tyr Asn Tyr Ala Glu Asp Tyr Gly Lys Gly  
195 200 205

Asp Thr Gly Ile Thr Val Glu Glu Ile Phe Lys Lys Ala Asn Asp Glu  
210 215 220

Tyr Trp Glu Pro Gly Glu Asp Arg Phe Ile Lys Ser Arg Tyr Glu Val  
225 230 235 240

Ala Ala Lys Leu Tyr Glu Glu Met Phe Gly Pro Asn Gly Pro Gln Thr  
245 250 255

Glu Glu Glu Leu Glu Ala Met Pro Asp Ala Ala Thr Arg Tyr Lys Thr  
260 265 270

Trp Lys Glu Gln Gln Lys Glu Asp Pro Ala Ser Asn Leu Pro Ser Tyr  
275 280 285

Asp Val Val Asp Ser Gly Lys Glu Tyr Asp Ile Tyr Asn Ile Ile Gly  
290 295 300

Asp Pro Glu Ser Phe Lys Lys Phe Arg Met Lys Gln Pro Pro Ile Ala  
305 310 315 320

Tyr Trp Leu Glu Thr Lys Lys Gly Arg Lys Gly Trp Leu Gln Lys Tyr  
325 330 335

## BCS 03-5005\_PCT-SEQUENZPROTOKOLL.ST25

Met Pro Ala Leu Pro His Gly Ser Lys Tyr Arg Val Tyr Phe Asn Thr  
 340 345 350

Pro Asn Gly Pro Leu Glu Arg Val Pro Ala Trp Ala Asn Phe Val Ile  
 355 360 365

Pro Asp Ala Gly Gly Met Ala Leu Ala Val His Trp Glu Pro Pro Pro  
 370 375 380

Glu Tyr Ala Tyr Lys Trp Lys His Lys Leu Pro Val Lys Pro Lys Ser  
 385 390 395 400

Leu Arg Ile Tyr Glu Cys His Val Gly Ile Ser Gly Gln Glu Pro Lys  
 405 410 415

Val Ser Ser Phe Asn Asp Phe Ile Ser Lys Val Leu Pro His Val Lys  
 420 425 430

Glu Ala Gly Tyr Asn Ala Ile Gln Ile Ile Gly Val Val Glu His Lys  
 435 440 445

Asp Tyr Phe Thr Val Gly Tyr Arg Val Thr Asn Phe Tyr Ala Val Ser  
 450 455 460

Ser Arg Tyr Gly Thr Pro Asp Asp Phe Lys Arg Leu Val Asp Glu Ala  
 465 470 475 480

His Gly Leu Gly Leu Leu Val Phe Leu Glu Ile Val His Ser Tyr Ala  
 485 490 495

Ala Ala Asp Glu Met Val Gly Leu Ser Leu Phe Asp Gly Ala Asn Asp  
 500 505 510

Cys Tyr Phe His Thr Gly Lys Arg Gly His His Lys Phe Trp Gly Thr  
 515 520 525

Arg Met Phe Lys Tyr Gly Asp Leu Asp Val Leu His Phe Leu Leu Ser  
 530 535 540

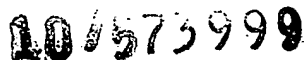
Asn Leu Asn Trp Trp Val Glu Glu Tyr His Val Asp Gly Phe His Phe  
 545 550 555 560

His Ser Leu Ser Ser Met Leu Tyr Thr His Asn Gly Phe Ala Ser Phe  
 565 570 575

Thr Gly Asp Met Asp Glu Tyr Cys Asn Gln Tyr Val Asp Lys Glu Ala  
 580 585 590

Leu Leu Tyr Leu Ile Leu Ala Asn Glu Val Leu His Ala Leu His Pro  
 595 600 605





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17/18  
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Gln Asn Ile Gln Arg Thr Ile Ser Arg Arg Ala Asp Gly Met Arg Phe  
865 870 875 880

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Cys Leu Glu Val Pro Leu Pro Ser Arg Ser Ala Gln Val Tyr Lys Leu  
885 890 895

Thr Arg Ile Leu Arg Ala  
900